SEQUENCE LISTING

<110>   Shinoda, Tetsuro
        Itoyama, Kyo
        Hamamura, Tetsuzo

<120>   JUVENILE HORMONE ACID METHYLTRANSFERASE
        GENES AND METHODS OF USING SAME

<130>   480230.401USPC

<140> US 10/542,867
<141> 2003-01-20

<150> PCT/JP03/00415
<151> 2003-01-20

<160>   38

<170>   PatentIn version 3.1

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aaaa atg aac aat gca gat tta tac cgc aaa agt aac agc ctc caa aag   169
     Met Asn Asn Ala Asp Leu Tyr Arg Lys Ser Asn Ser Leu Gln Lys
      1   5   10   15

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Arg Asp Ala Leu Arg Cys Leu Glu Glu His Ala Asn Lys Ile Lys Trp
                20   25   30

aaa aaa atc ggt gat aga gtc ata gat ttg ggt tgc gct gac ggt agt   265
Lys Lys Ile Gly Asp Arg Val Ile Asp Leu Gly Cys Ala Asp Gly Ser
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gtt act gat att ttg aaa gtt tac atg cca aaa aat tac gga aga tta   313
Val Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu
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    65                  70                  75

cac ggc ttc ggt agg act tcg ttc agg gtg ctc gac ata gag ggc gat      409
His Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp
80                  85                  90                  95

ttg acc gca gac ctg aaa caa ggc ttt gat cac gtt ttc tct ttt tac      457
Leu Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr
                100                 105                 110

acc ctc cac tgg atc aga gac cag gaa cga gct ttc cgg aac att ttc      505
Thr Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe
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act cct atc ttt gat gtt tac cgc aca ctc tcg cat aca gaa aaa tgg      601
Thr Pro Ile Phe Asp Val Tyr Arg Thr Leu Ser His Thr Glu Lys Trp
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cat tct tgg ctc gag cac gtc gat cga ttt ata tca cct tac cat gac      649
His Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp
160                 165                 170                 175

aat gaa gat ccc gaa aaa gaa gtt aag aag ata atg gaa aga gtt gga      697
Asn Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly
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ttt agc aat att gaa gtg caa tgc aaa acg ttg ttc tat gta tac gat      745
Phe Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp
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gat ttg gat gtt tta aaa aaa tca gta gca gct atc aat cca ttt aat      793
Asp Leu Asp Val Leu Lys Lys Ser Val Ala Ala Ile Asn Pro Phe Asn
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atc ccg aaa gac ata ctt gaa gac ttt tta gaa gat tac ata gat gta      841
Ile Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val
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gta cgg gag atg agg ctg ctc gac agg tgt aat aac aat gtc ggt gaa      889
Val Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Asn Val Gly Glu
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tca gtg tct ata aaa ttt aac tac aaa gtc atc agt gtt tac gcg aga      937
Ser Val Ser Ile Lys Phe Asn Tyr Lys Val Ile Ser Val Tyr Ala Arg
                260                 265                 270

aaa tta tgt tta agt tta atg taa ttaagttaga aaaaaaaaac aaatccgact     991
Lys Leu Cys Leu Ser Leu Met
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gatggcggtg ttgtacgact taaagtgttg agaatttaaa ataatttcta cggttgttaa   1951

attataattg aaatagaaat ccatactatt ttaattactc aactcaacaa ctcaattatt   2011

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gctgatttct ttttcattat atccgtaaat tttaggacaa gttttgtacc accaactaca   2131

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ttttagtgag aattacatga aacaaattat gaaacaaagt ttgattatac tttcaaatgt   2491

ttcattactg ttttttaagct taaggtataa aatggcatgt ttgtgtgttt actcaggccc   2551

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ttattgacaa cataattagt aaaacatgtg ataatttgaa caatgacaaa tttattgtta    2791

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Lys Ile Gly Asp Arg Val Ile Asp Leu Gly Cys Ala Asp Gly Ser Val
            35                  40                  45

Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu Val
        50                  55                  60

Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His His
65                  70                  75                  80

Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp Leu
                85                  90                  95

Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr Thr
            100                 105                 110

Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe Asn
            115                 120                 125

Leu Leu Gly Asp Glu Gly Asp Cys Leu Leu Leu Phe Leu Gly His Thr
        130                 135                 140

Pro Ile Phe Asp Val Tyr Arg Thr Leu Ser His Thr Glu Lys Trp His
145                 150                 155                 160

Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp Asn
                165                 170                 175

Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly Phe
            180                 185                 190
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Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp Asp
        195                 200                 205

Leu Asp Val Leu Lys Lys Ser Val Ala Ala Ile Asn Pro Phe Asn Ile
        210                 215                 220

Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val Val
225                 230                 235                 240

Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Asn Val Gly Glu Ser
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gat gcc aaa ttg att ctg gat gag ttc gca tcg acc atg cag tgg cga      96
Asp Ala Lys Leu Ile Leu Asp Glu Phe Ala Ser Thr Met Gln Trp Arg
                20                  25                  30

tcc gat gga gag gat gcc ctc ctg gat gtg ggt tca gga tct ggt aac     144
Ser Asp Gly Glu Asp Ala Leu Leu Asp Val Gly Ser Gly Ser Gly Asn
            35                  40                  45

gtg ctc atg gac ttt gta aag cca ctg ctc ccg att cgt gga caa ctg     192
Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu
    50                  55                  60

gtg ggc aca gac atc tcc agc cag atg gtg cac tat gcc agt aag cat     240
Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His
65                  70                  75                  80

tac cag cga gag gag cgt acc aga ttc cag gtt ctg gac att gga tgc     288
Tyr Gln Arg Glu Glu Arg Thr Arg Phe Gln Val Leu Asp Ile Gly Cys
                85                  90                  95
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gaa cgg ctg ccc gag gag ctg agc ggc aga ttt gac cat gtc acc tcg          336
Glu Arg Leu Pro Glu Glu Leu Ser Gly Arg Phe Asp His Val Thr Ser
            100                 105                 110

ttc tac tgc ctc cat tgg gtg caa aat ctg aaa gga gct ctc gga aat          384
Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn
            115                 120                 125

atc tac aat ctt ctg aag ccc gaa ggt ggc gac tgc ctc ctg gca ttt          432
Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe
        130                 135                 140

ttg gcc tcc aat ccg gtt tac gaa gtc tat aag att ctt aaa acg aat          480
Leu Ala Ser Asn Pro Val Tyr Glu Val Tyr Lys Ile Leu Lys Thr Asn
145                 150                 155                 160

gac aag tgg tcg act tat atg cag gat gtg gag aac ttc ata tcc cca          528
Asp Lys Trp Ser Thr Tyr Met Gln Asp Val Glu Asn Phe Ile Ser Pro
                165                 170                 175

ctt cac tac agt cta aat cct ggc gag gaa ttc agc cag ttg ttg aac          576
Leu His Tyr Ser Leu Asn Pro Gly Glu Glu Phe Ser Gln Leu Leu Asn
            180                 185                 190

gat gtg ggt ttc gtg caa cac aat gtg gaa att cga aac gaa gtg ttt          624
Asp Val Gly Phe Val Gln His Asn Val Glu Ile Arg Asn Glu Val Phe
            195                 200                 205

gtt tat gaa ggt gta agg act ctg aaa gat aat gta aag gcc att tgt          672
Val Tyr Glu Gly Val Arg Thr Leu Lys Asp Asn Val Lys Ala Ile Cys
        210                 215                 220

cct ttt ctt gag cga atg cct gca gat ttg cat gaa cag ttc ctg gat          720
Pro Phe Leu Glu Arg Met Pro Ala Asp Leu His Glu Gln Phe Leu Asp
225                 230                 235                 240

gac ttc ata gac att gtt ata tcc atg aat ttg cag caa ggt gaa aat          768
Asp Phe Ile Asp Ile Val Ile Ser Met Asn Leu Gln Gln Gly Glu Asn
                245                 250                 255

aat gag gat caa aag ttc cta tct ccc tat aaa ctg gtg gtg gcc tat          816
Asn Glu Asp Gln Lys Phe Leu Ser Pro Tyr Lys Leu Val Val Ala Tyr
            260                 265                 270

gct cgc aag act cct gaa ttt gtg aat aat gtt ttc ctg gag cct aca          864
Ala Arg Lys Thr Pro Glu Phe Val Asn Asn Val Phe Leu Glu Pro Thr
            275                 280                 285

cat caa aac ttg gtt aag gga ata aat taa ttttatttta caaattaaca           914
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<213>   Drosophila melanogaster

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Ser Asp Gly Glu Asp Ala Leu Leu Asp Val Gly Ser Gly Ser Gly Asn
            35                  40                  45

Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu
    50                  55                  60

Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His
65                  70                  75                  80

Tyr Gln Arg Glu Glu Arg Thr Arg Phe Gln Val Leu Asp Ile Gly Cys
            85                  90                  95

Glu Arg Leu Pro Glu Glu Leu Ser Gly Arg Phe Asp His Val Thr Ser
            100                 105                 110

Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn
        115                 120                 125

Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe
    130                 135                 140

Leu Ala Ser Asn Pro Val Tyr Glu Val Tyr Lys Ile Leu Lys Thr Asn
145                 150                 155                 160

Asp Lys Trp Ser Thr Tyr Met Gln Asp Val Glu Asn Phe Ile Ser Pro
            165                 170                 175

Leu His Tyr Ser Leu Asn Pro Gly Glu Glu Phe Ser Gln Leu Leu Asn
        180                 185                 190

Asp Val Gly Phe Val Gln His Asn Val Glu Ile Arg Asn Glu Val Phe
        195                 200                 205

Val Tyr Glu Gly Val Arg Thr Leu Lys Asp Asn Val Lys Ala Ile Cys
    210                 215                 220

Pro Phe Leu Glu Arg Met Pro Ala Asp Leu His Glu Gln Phe Leu Asp
225                 230                 235                 240

Asp Phe Ile Asp Ile Val Ile Ser Met Asn Leu Gln Gln Gly Glu Asn
            245                 250                 255
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Asn Glu Asp Gln Lys Phe Leu Ser Pro Tyr Lys Leu Val Val Ala Tyr
        260             265             270
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1               5                   10                  15
```

```
gat gcg atg gag ata ttg aaa gaa tac gca cca ctc atc agc tgt cca      96
Asp Ala Met Glu Ile Leu Lys Glu Tyr Ala Pro Leu Ile Ser Cys Pro
            20                  25                  30
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agg gat ggc gaa gag gtt gcc ctg tta gac att ggg tgt ggc agc ggg     144
Arg Asp Gly Glu Glu Val Ala Leu Leu Asp Ile Gly Cys Gly Ser Gly
        35                  40                  45
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gac gtg ttg gtg gac tac att cta ccg gtg ctg agc cgc gga agc act     192
Asp Val Leu Val Asp Tyr Ile Leu Pro Val Leu Ser Arg Gly Ser Thr
        50                  55                  60
```

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cct gtg gcg cgc gca ttg gcg aca gac atc tcg gag cag atg gtg cgc     240
Pro Val Ala Arg Ala Leu Ala Thr Asp Ile Ser Glu Gln Met Val Arg
65                  70                  75                  80
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cat gca cgt gaa tcg tac cgt cac gtt aag acg atc gag ttc gac acc     288
His Ala Arg Glu Ser Tyr Arg His Val Lys Thr Ile Glu Phe Asp Thr
                85                  90                  95
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ctt gac atc ggc atc aaa ctc gat agt gca aag ttg tcc cgc tgg gga     336
Leu Asp Ile Gly Ile Lys Leu Asp Ser Ala Lys Leu Ser Arg Trp Gly
                100                 105                 110
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caa ttt agt cac gtt acc tcg ttc tac tgc cta cac tgg gtt cag aat     384
Gln Phe Ser His Val Thr Ser Phe Tyr Cys Leu His Trp Val Gln Asn
                115                 120                 125
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cag cac gta gcc ttt tcc aac atc tac aac ctt ctg cag cat ggc ggt        432
Gln His Val Ala Phe Ser Asn Ile Tyr Asn Leu Leu Gln His Gly Gly
    130                 135                 140

gac tgt ctg ctg gtg ttt ttg gca aac aac cca atc ttt gac ata tac        480
Asp Cys Leu Leu Val Phe Leu Ala Asn Asn Pro Ile Phe Asp Ile Tyr
145                 150                 155                 160

aac caa ctg tct cgc tca ccc aag tgg tcc aag tat atg tac gac gtg        528
Asn Gln Leu Ser Arg Ser Pro Lys Trp Ser Lys Tyr Met Tyr Asp Val
                165                 170                 175

gaa aag tac att tcg ccc tac cag tat tgt gaa aat cca gca agt gag        576
Glu Lys Tyr Ile Ser Pro Tyr Gln Tyr Cys Glu Asn Pro Ala Ser Glu
                180                 185                 190

atc gag gat ctg ctg tgc acg gtg ggc ttt cag cag tat cag ata cag        624
Ile Glu Asp Leu Leu Cys Thr Val Gly Phe Gln Gln Tyr Gln Ile Gln
            195                 200                 205

gtt cgc gac aag ctg tac gtg tac gaa ggg ctg gac aat ttg aaa cga        672
Val Arg Asp Lys Leu Tyr Val Tyr Glu Gly Leu Asp Asn Leu Lys Arg
    210                 215                 220

gca gtt ttg gct gtg aat cca ttc agt gaa cga atg cca cca gaa ctg        720
Ala Val Leu Ala Val Asn Pro Phe Ser Glu Arg Met Pro Pro Glu Leu
225                 230                 235                 240

cag gat agg ttc cta ctg gac tat atc gct gtt gtg cgg cag atg tac        768
Gln Asp Arg Phe Leu Leu Asp Tyr Ile Ala Val Val Arg Gln Met Tyr
                245                 250                 255

ttg acc aaa act ggc agc gaa gag aat gat tgc aat ctt caa ttc ata        816
Leu Thr Lys Thr Gly Ser Glu Glu Asn Asp Cys Asn Leu Gln Phe Ile
                260                 265                 270

tcc cca tac aag ttg gtg gtt gtt tat gcg aag aaa taa                    855
Ser Pro Tyr Lys Leu Val Val Val Tyr Ala Lys Lys
            275                 280


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<212>   PRT
<213>   Anopheles gambiae

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1               5                   10                  15

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            20                  25                  30

Arg Asp Gly Glu Glu Val Ala Leu Leu Asp Ile Gly Cys Gly Ser Gly
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            35                        40                        45
Asp Val Leu Val Asp Tyr Ile Leu Pro Val Leu Ser Arg Gly Ser Thr
    50                    55                    60

Pro Val Ala Arg Ala Leu Ala Thr Asp Ile Ser Glu Gln Met Val Arg
65                    70                    75                    80

His Ala Arg Glu Ser Tyr Arg His Val Lys Thr Ile Glu Phe Asp Thr
                85                    90                    95

Leu Asp Ile Gly Ile Lys Leu Asp Ser Ala Lys Leu Ser Arg Trp Gly
                100                   105                   110

Gln Phe Ser His Val Thr Ser Phe Tyr Cys Leu His Trp Val Gln Asn
            115                   120                   125

Gln His Val Ala Phe Ser Asn Ile Tyr Asn Leu Leu Gln His Gly Gly
    130                   135                   140

Asp Cys Leu Leu Val Phe Leu Ala Asn Asn Pro Ile Phe Asp Ile Tyr
145                   150                   155                   160

Asn Gln Leu Ser Arg Ser Pro Lys Trp Ser Lys Tyr Met Tyr Asp Val
                165                   170                   175

Glu Lys Tyr Ile Ser Pro Tyr Gln Tyr Cys Glu Asn Pro Ala Ser Glu
                180                   185                   190

Ile Glu Asp Leu Leu Cys Thr Val Gly Phe Gln Gln Tyr Gln Ile Gln
                195                   200                   205

Val Arg Asp Lys Leu Tyr Val Tyr Glu Gly Leu Asp Asn Leu Lys Arg
    210                   215                   220

Ala Val Leu Ala Val Asn Pro Phe Ser Glu Arg Met Pro Pro Glu Leu
225                   230                   235                   240

Gln Asp Arg Phe Leu Leu Asp Tyr Ile Ala Val Val Arg Gln Met Tyr
                245                   250                   255

Leu Thr Lys Thr Gly Ser Glu Glu Asn Asp Cys Asn Leu Gln Phe Ile
                260                   265                   270

Ser Pro Tyr Lys Leu Val Val Val Tyr Ala Lys Lys
        275                   280
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<213>   Spodoptera litura

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                                                        Met Asn
                                                          1

aac gcc gtt ttg tac gaa caa gct aac agc atg cag aag aga gat gca        164
Asn Ala Val Leu Tyr Glu Gln Ala Asn Ser Met Gln Lys Arg Asp Ala
         5                   10                  15

ctc aac ttt tta gac gac atc tcc cct aaa cta aag tgg aag aag agt        212
Leu Asn Phe Leu Asp Asp Ile Ser Pro Lys Leu Lys Trp Lys Lys Ser
     20                  25                  30

atc agc aac att ctg gac gta gga tgt gga gat gga tgt gtc acc agc        260
Ile Ser Asn Ile Leu Asp Val Gly Cys Gly Asp Gly Cys Val Thr Ser
35                  40                  45                  50

atg ctt aaa aag tac atc cct act gac ttc aag ctg ctc ggc tgt gac        308
Met Leu Lys Lys Tyr Ile Pro Thr Asp Phe Lys Leu Leu Gly Cys Asp
                 55                  60                  65

atc agt gag aag atg gtg aat ttc gcc aat gac cac cat tgc aat gaa        356
Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys Asn Glu
                 70                  75                  80

cag acg tcg ttc aca gtg ctg gac atc gca gga gat ata ccc gaa ggt        404
Gln Thr Ser Phe Thr Val Leu Asp Ile Ala Gly Asp Ile Pro Glu Gly
             85                  90                  95

atg aag gga aaa ttc gac cat gtt ttc tcc ttc tat gcc ttg cac tgg        452
Met Lys Gly Lys Phe Asp His Val Phe Ser Phe Tyr Ala Leu His Trp
         100                 105                 110

gtc ttg gat caa gag cgc gta ttc agg aat att tac gat ttg ctg agt        500
Val Leu Asp Gln Glu Arg Val Phe Arg Asn Ile Tyr Asp Leu Leu Ser
115                 120                 125                 130

aaa gat gga gaa tgc ttc acg ata ttt gtc gca ggc gca ccc gtg ttc        548
Lys Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Gly Ala Pro Val Phe
                 135                 140                 145

gac ttg tac cgc att tta tcg cgt aac aac aaa tgg agc act ctg ctt        596
Asp Leu Tyr Arg Ile Leu Ser Arg Asn Asn Lys Trp Ser Thr Leu Leu
             150                 155                 160

aaa gat gtc gag aaa tac ata tcg cca tac cac gac tca cag gat cca        644
Lys Asp Val Glu Lys Tyr Ile Ser Pro Tyr His Asp Ser Gln Asp Pro
             165                 170                 175
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gcg aaa gaa atg aga aaa gta ttg gaa aaa gtt gga tac gtg gac tac     692
Ala Lys Glu Met Arg Lys Val Leu Glu Lys Val Gly Tyr Val Asp Tyr
    180                 185                 190

aag gtg gaa tgt aaa aac ttg gtg tat atg tac aac aac ttc gcc agt     740
Lys Val Glu Cys Lys Asn Leu Val Tyr Met Tyr Asn Asn Phe Ala Ser
195                 200                 205                 210

tta tgg aaa acc ctt caa gca atc aac cca ttc aac atc ccg aaa gat     788
Leu Trp Lys Thr Leu Gln Ala Ile Asn Pro Phe Asn Ile Pro Lys Asp
                215                 220                 225

atg gaa gaa gat ttc aaa caa gat tac tta aat att tta aaa gat atg     836
Met Glu Glu Asp Phe Lys Gln Asp Tyr Leu Asn Ile Leu Lys Asp Met
                230                 235                 240

aaa att gtg tct aag tat aat acc gat gag gca agt gtg aac ttc aaa     884
Lys Ile Val Ser Lys Tyr Asn Thr Asp Glu Ala Ser Val Asn Phe Lys
        245                 250                 255

tat cgg ttg ctt gtc gta cac gct cgc aag ccg gcc tca gaa ttt tag     932
Tyr Arg Leu Leu Val Val His Ala Arg Lys Pro Ala Ser Glu Phe
    260                 265                 270

ggaaaataat cacaaataaa ctaactgaat atttgtagta caataacaaa acctgatgca   992

ag                                                                  994


<210>  8
<211>  273
<212>  PRT
<213>  Spodoptera litura

<400>  8
Met Asn Asn Ala Val Leu Tyr Glu Gln Ala Asn Ser Met Gln Lys Arg
1               5                   10                  15

Asp Ala Leu Asn Phe Leu Asp Asp Ile Ser Pro Lys Leu Lys Trp Lys
                20                  25                  30

Lys Ser Ile Ser Asn Ile Leu Asp Val Gly Cys Gly Asp Gly Cys Val
            35                  40                  45

Thr Ser Met Leu Lys Lys Tyr Ile Pro Thr Asp Phe Lys Leu Leu Gly
        50                  55                  60

Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys
65                  70                  75                  80

Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Ala Gly Asp Ile Pro
                85                  90                  95
```

```
Glu Gly Met Lys Gly Lys Phe Asp His Val Phe Ser Phe Tyr Ala Leu
        100             105             110

His Trp Val Leu Asp Gln Glu Arg Val Phe Arg Asn Ile Tyr Asp Leu
        115             120             125

Leu Ser Lys Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Gly Ala Pro
    130             135             140

Val Phe Asp Leu Tyr Arg Ile Leu Ser Arg Asn Asn Lys Trp Ser Thr
145             150             155             160

Leu Leu Lys Asp Val Glu Lys Tyr Ile Ser Pro Tyr His Asp Ser Gln
        165             170             175

Asp Pro Ala Lys Glu Met Arg Lys Val Leu Glu Lys Val Gly Tyr Val
        180             185             190

Asp Tyr Lys Val Glu Cys Lys Asn Leu Val Tyr Met Tyr Asn Asn Phe
        195             200             205  .

Ala Ser Leu Trp Lys Thr Leu Gln Ala Ile Asn Pro Phe Asn Ile Pro
    210             215             220

Lys Asp Met Glu Glu Asp Phe Lys Gln Asp Tyr Leu Asn Ile Leu Lys
225             230             235             240

Asp Met Lys Ile Val Ser Lys Tyr Asn Thr Asp Glu Ala Ser Val Asn
        245             250             255

Phe Lys Tyr Arg Leu Leu Val Val His Ala Arg Lys Pro Ala Ser Glu
        260             265             270

Phe


<210>   9
<211>   1193
<212>   DNA
<213>   Helicoverpa armigera

<220>
<221>   CDS
<222>   (124)..(978)
<223>

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aagaatcata aactaaacaa atcaatatca cgaaattcaa atacctataa aaaaatcctt     120

aaa atg aat aac gcg gtc ttg tat gaa aaa agc aat agc ttg cag aag     168
    Met Asn Asn Ala Val Leu Tyr Glu Lys Ser Asn Ser Leu Gln Lys
    1               5               10              15
```

```
aga gat gct atc atg tgt cta gaa gaa tac gct tcg aaa att aag tgg          216
Arg Asp Ala Ile Met Cys Leu Glu Glu Tyr Ala Ser Lys Ile Lys Trp
                20                  25                  30

aag aag agt aat aat aat att ctt gac ata ggc tgt ggg gat gga agc          264
Lys Lys Ser Asn Asn Asn Ile Leu Asp Ile Gly Cys Gly Asp Gly Ser
                35                  40                  45

gtg act aat atg ctg aag aaa tac atc cct act gag tac aag ttg ctt          312
Val Thr Asn Met Leu Lys Lys Tyr Ile Pro Thr Glu Tyr Lys Leu Leu
                50                  55                  60

ggc tgt gat att agc gag aag atg gtg aac ttc gcg aat gat cat cat          360
Gly Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His
    65                  70                  75

tgt aac gaa cag act tct ttc acc gtg ctc gat att gag gga gac cta          408
Cys Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Glu Gly Asp Leu
80                  85                  90                  95

cct gaa ggt atg aag gga aac ttc gac cac gtt ttc tcg ttc tac gct          456
Pro Glu Gly Met Lys Gly Asn Phe Asp His Val Phe Ser Phe Tyr Ala
                100                 105                 110

ctg cac tgg gtt aat aac caa gaa cga gca ttc aaa aac ata tac aac          504
Leu His Trp Val Asn Asn Gln Glu Arg Ala Phe Lys Asn Ile Tyr Asn
                115                 120                 125

ctt cta agc gag gat ggg gag tgc ttc acg ata ttc gta gcc tgg gct          552
Leu Leu Ser Glu Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Trp Ala
                130                 135                 140

cct gtg ttt gac gtg tac cga gtg ctc gcg cgc aac aac aag tgg agt          600
Pro Val Phe Asp Val Tyr Arg Val Leu Ala Arg Asn Asn Lys Trp Ser
    145                 150                 155

caa tgg gtg cat gat gtc gac aga tac ata tcg ccc tac cac gac tct          648
Gln Trp Val His Asp Val Asp Arg Tyr Ile Ser Pro Tyr His Asp Ser
160                 165                 170                 175

ttg gag ccg gaa aaa gat tta aag gct atg ata gac aaa att gga ttc          696
Leu Glu Pro Glu Lys Asp Leu Lys Ala Met Ile Asp Lys Ile Gly Phe
                180                 185                 190

gtt gac atc gat gtg gaa tgt aaa gaa ttg gta ttc gtg tac gac aac          744
Val Asp Ile Asp Val Glu Cys Lys Glu Leu Val Phe Val Tyr Asp Asn
                195                 200                 205

ata cat att ttg cga aaa gcg tta aca gca atc aac cct ttc aaa atc          792
Ile His Ile Leu Arg Lys Ala Leu Thr Ala Ile Asn Pro Phe Lys Ile
                210                 215                 220

ccc aag gaa aaa tat gat gat ttc atg gaa gac tat atg gat ata ctg          840
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Pro Lys Glu Lys Tyr Asp Asp Phe Met Glu Asp Tyr Met Asp Ile Leu
    225             230             235

aaa gaa cta caa att tta gac aag tac aac aat aat tat gaa aag agc       888
Lys Glu Leu Gln Ile Leu Asp Lys Tyr Asn Asn Asn Tyr Glu Lys Ser
240             245             250             255

gtt gaa ttc aat tac cgt ttg ctt gta gtg tat gcc cga aaa cct gac       936
Val Glu Phe Asn Tyr Arg Leu Leu Val Val Tyr Ala Arg Lys Pro Asp
                260             265             270

tcg cag gat aaa atg tta gaa gct cta aat gga caa acg tag             978
Ser Gln Asp Lys Met Leu Glu Ala Leu Asn Gly Gln Thr
                275             280

actgaaaaac ttatattttt agttacggca aaatacagtg tagaacagtt atttgtagtt      1038

aaggatgaat gtatagtgta tctcttcagg tttagttttg ggcctggtat gaaatgttgt      1098

ttttttaagt aagctatttt ggtaatgtaa actattttta aaggcaggaa ataatctgt       1158

gtgtgagcaa aaaaaaaaaa aaaaaaaaaa aaaaa                                  1193


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<211>  284
<212>  PRT
<213>  Helicoverpa armigera

<400>  10
Met Asn Asn Ala Val Leu Tyr Glu Lys Ser Asn Ser Leu Gln Lys Arg
1               5               10              15

Asp Ala Ile Met Cys Leu Glu Glu Tyr Ala Ser Lys Ile Lys Trp Lys
                20              25              30

Lys Ser Asn Asn Asn Ile Leu Asp Ile Gly Cys Gly Asp Gly Ser Val
            35              40              45

Thr Asn Met Leu Lys Lys Tyr Ile Pro Thr Glu Tyr Lys Leu Leu Gly
    50              55              60

Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys
65              70              75              80

Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Glu Gly Asp Leu Pro
                85              90              95

Glu Gly Met Lys Gly Asn Phe Asp His Val Phe Ser Phe Tyr Ala Leu
            100             105             110

His Trp Val Asn Asn Gln Glu Arg Ala Phe Lys Asn Ile Tyr Asn Leu
            115             120             125
```

```
Leu Ser Glu Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Trp Ala Pro
    130             135             140
```

```
Val Phe Asp Val Tyr Arg Val Leu Ala Arg Asn Asn Lys Trp Ser Gln
145             150             155             160
```

```
Trp Val His Asp Val Asp Arg Tyr Ile Ser Pro Tyr His Asp Ser Leu
            165             170             175
```

```
Glu Pro Glu Lys Asp Leu Lys Ala Met Ile Asp Lys Ile Gly Phe Val
            180             185             190
```

```
Asp Ile Asp Val Glu Cys Lys Glu Leu Val Phe Val Tyr Asp Asn Ile
            195             200             205
```

```
His Ile Leu Arg Lys Ala Leu Thr Ala Ile Asn Pro Phe Lys Ile Pro
    210             215             220
```

```
Lys Glu Lys Tyr Asp Asp Phe Met Glu Asp Tyr Met Asp Ile Leu Lys
225             230             235             240
```

```
Glu Leu Gln Ile Leu Asp Lys Tyr Asn Asn Asn Tyr Glu Lys Ser Val
            245             250             255
```

```
Glu Phe Asn Tyr Arg Leu Leu Val Val Tyr Ala Arg Lys Pro Asp Ser
            260             265             270
```

```
Gln Asp Lys Met Leu Glu Ala Leu Asn Gly Gln Thr
            275             280
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<210>  11
<211>  17
<212>  DNA
<213>  Artificial

<220>
<223>  an artificially synthesized primer sequence

<400>  11
tttttttttt tttttgc                                                    17


<210>  12
<211>  10
<212>  DNA
<213>  Artificial

<220>
<223>  an artificially synthesized primer sequence

<400>  12
gatcatagcc                                                            10
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<210>   13
<211>   25
<212>   DNA
<213>   Artificial

<220>
<223>   an artificially synthesized primer sequence

<400>   13
aagccgcagt aagatggcgg tgttg                                            25


<210>   14
<211>   25
<212>   DNA
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<220>
<223>  an artificially synthesized primer sequence

<400>   14
caacaccgcc atcttactgc ggctt                                            25


<210>   15
<211>   30
<212>   DNA
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<220>
<223>   an artificially synthesized primer sequence

<400>   15
aaacatatga acaatgcaga tttataccgc                                       30


<210>   16
<211>   30
<212>   DNA
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<220>
<223>   an artificially synthesized primer sequence

<400>   16
aaggatccaa tcacgaaaat ctgggaagac                                       30


<210>   17
<211>   30
<212>   DNA
<213>   Artificial
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<220>
<223>   an artificially synthesized primer sequence

<400>   17
aaacatatga atcaggcctc tctatatcag   30

<210>   18
<211>   34
<212>   DNA
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<400>   18
aaggatccga ctctgttaac aaatgcaatt actg   34

<210>   19
<211>   23
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<220>
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<222>   (6)..(6)
<223>   "n"=A,T,G or C

<220>
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<222>   (15)..(15)
<223>   "n"=A,T,G or C

<400>   19
atggtnaart aygcnaayaa rca   23

<210>   20
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<223>   "n"=A,T,G or C

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<220>
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<222>  (12)..(12)
<223>  "n"=A,T,G or C

<400>  20
taraangara anacrtgrtc raa                                      23


<210>  21
<211>  28
<212>  DNA
<213>  Artificial

<220>
<223>  an artificially synthesized primer sequence

<400>  21
ttcacagtgc tggacatcgc aggagata                                 28


<210>  22
<211>  28
<212>  DNA
<213>  Artificial

<220>
<223>  an artificially synthesized primer sequence

<400>  22
tatctcctgc gatgtccagc actgtgaa                                 28


<210>  23
<211>  26
<212>  DNA
<213>  Artificial

<220>
<223>  an artificially synthesized primer sequence

<400>  23
cgaacagact tctttcaccg tgctcg                                   26


<210>  24
<211>  26
<212>  DNA
<213>  Artificial

<220>
<223>  an artificially synthesized primer sequence

<400>  24
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cgagcacggt gaaagaagtc tgttcg   26

<210> 25
<211> 30
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 25
aaacatatga ataacgccgt tttgtacgaa   30

<210> 26
<211> 30
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 26
aactcgagct tgcatcaggt tttgttattg   30

<210> 27
<211> 30
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 27
aaacatatga ataacgcggt cttgtatgaa   30

<210> 28
<211> 30
<212> DNA
<213> Artificial

<220>
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<400> 28
aactcgaggc ccaaaactaa acctgaagag   30

<210> 29
<211> 8
<212> PRT

<213> Artificial

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> "Xaa"=Asp or Glu

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> "Xaa"=hydrophobic amino acid

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> "Xaa"=low molecular weight neutral amino acid

<220>
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<222> (7)..(7)
<223> "Xaa"=low molecular weight neutral amino acid

<400> 29
Leu Xaa Xaa Gly Xaa Gly Xaa Gly
1   5

<210> 30
<211> 18
<212> PRT
<213> Artificial

<220>
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<220>
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<222> (5)..(5)
<223> "Xaa"=any amino acid

<220>
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<222> (8)..(8)
<223> "Xaa"=Gln or Glu

<220>
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<222> (9)..(9)
<223> "Xaa"=His, Lys or Gln

<220>

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<221>  MISC_FEATURE
<222>  (13)..(13)
<223>  "Xaa"=hydrophobic amino acid

<400>  30
Met Asn Asn Ala Xaa Leu Tyr Xaa Xaa Ala Asn Ser Xaa Gln Lys Arg
1               5                   10                  15

Asp Ala


<210>  31
<211>  9
<212>  PRT
<213>  Artificial

<220>
<223>  consensus sequence

<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  "Xaa"=Leu, Val or Ile

<220>
<221>  MISC_FEATURE
<222>  (4)..(4)
<223>  "Xaa"=Leu, Val or Ile

<400>  31
Xaa Leu Asp Xaa Gly Cys Gly Asp Gly
1               5


<210>  32
<211>  12
<212>  PRT
<213>  Artificial

<220>
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<220>
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<222>  (1)..(1)
<223>  "Xaa"=Gln, Arg or Lys

<220>
<221>  MISC_FEATURE
<222>  (3)..(3)
<223>  "Xaa"=Leu or Val

<220>
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<221>  MISC_FEATURE
<222>  (10)..(10)
<223>  "Xaa"=Gln or Lys

<400>  32
Xaa Leu Xaa Gly Cys Asp Ile Ser Glu Xaa Met Val
1               5                   10


<210>  33
<211>  13
<212>  PRT
<213>  Artificial

<220>
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<220>
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<222>  (9)..(9)
<223>  "Xaa"=Cys, Thr or Ala

<400>  33
Phe Asp His Val Phe Ser Phe Tyr Xaa Leu His Trp Val
1               5                   10


<210>  34
<211>  9
<212>  PRT
<213>  Artificial

<220>
<223>  consensus sequence

<220>
<221>  MISC_FEATURE
<222>  (2)..(2)
<223>  "Xaa"=Val or Ile

<220>
<221>  MISC_FEATURE
<222>  (5)..(5)
<223>  "Xaa"=Val, Ile or Leu

<220>
<221>  MISC_FEATURE
<222>  (8)..(8)
<223>  "Xaa"=Ile or Val

<400>  34
Pro Xaa Phe Asp Xaa Tyr Arg Xaa Leu
1               5
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<210> 35
<211> 12
<212> PRT
<213> Artificial

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> "Xaa"=Lys or Arg

<400> 35
Asp Val Glu Xaa Tyr Ile Ser Pro Tyr His Asp Ser
1   5   10

<210> 36
<211> 10
<212> PRT
<213> Artificial

<220>
<223> consensus sequence

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<222> (4)..(4)
<223> "Xaa"=Ile, Val or Leu

<400> 36
Tyr Lys Leu Xaa Val Val Tyr Ala Arg Lys
1   5   10

<210> 37
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence encoded from DGJF primer

<400> 37
Met Val Lys Tyr Ala Asn Lys His
 1   5

<210> 38
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence encoded from DGJR primer

<400> 38
Phe Asp His Val Phe Ser Phe Tyr
 1   5